

		2661		2730
humPMS2	(2574)	CATTTCAGAAC	-----	
AtPMS2	(2267)	CTTTACTCACTTACCTGATGACGACAATGTCAATGATGATGATGATGATGCAACCATCTCATTGGC		
Consensus	(2661)	C TT CTCA A		
		2731		
humPMS2	(2587)	----		
AtPMS2	(2337)	ATGA		
Consensus	(2731)			

Figure 1. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) DNA sequences. Similarity is 48.1%; identity is 48.1%. Black boxes show identical nucleotides.

003327-10564260

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1                                     70
humPMS2 (1) --MERABSSSEPAKAIKPIDRKSVHICSGQVILSLSTAVKELVENS LDAGATNIDLKIKDYGV LIEV
AtPMS2 (1) MQGDSSSPPTTSSPLIRPINRNVIRICSGQVILDLSSAVKELVENS LDAGATSI EINLRDYGEYFQV
Consensus (1) D A S ST A IKPI R IH IC SGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V
71                                     140
humPMS2 (69) SDNGCCVEEBNF-----EGLTLHTSKIQEADTQVEFGFRGEALSSLCALSDV LISA CHA
AtPMS2 (71) IDNGCCISPTNRKVCQILRRTFDVLALHTSKLEDTIDLNLTTFYGFGEALSSLCALGNLIVE RTK
Consensus (71) DNGCGI NF D L LKHTSKI DF DL NL TFGFRGEALSSLCAL LTI T
141                                     210
humPMS2 (128) SAKVCTRLMFDHNGKIIQKTPYPRGTTT SVQQLFSLTPVHKEEORNIKKEYAKMAOV LHA YCI SAS
AtPMS2 (141) NEPVATLITFDHSGLLTA EKKTARQICTTITVRKLFSLNPVSKKEKRNIRKEYGKLVSLNAYALAKG
Consensus (141) VAT L FDH G I R GTTVSV LFS LPVR KEF RNIKKEYAKLV LL AY IIA G
211                                     280
humPMS2 (198) IRVSCITNQLCGKQRPVVCIGGSPSIRKNGSVFVGQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNL
AtPMS2 (211) VEFVCSNTTCKNPKSVVLNQCRCGLNPTITVFGISTFTSLCP-----
Consensus (211) IR CSN G K VL T G SIKDNI SVFG SL P
281                                     350
humPMS2 (268) YISGFISQCTHGVGRSSTDRQFFFINRECEPAKVCRLVNEVHMYNRHQYFFVVLNISVDSECVINVT
AtPMS2 (255) ---G-----TGRLADRCYFFINGREVDMPKVKSLVNEIKDTSRRKVPVTILDFIIPGGACINVT
Consensus (281) G DRQFFFIN RP D KV KLVNELY YP IL V DINVT
351                                     420
humPMS2 (338) PDKRQIILQEEKLLLA VLKTS LIGMFDSVKNLNVSQQLLDVEGNLIKMAADLEKPMVEKQDQSPSLR
AtPMS2 (314) PDKRKVFSDET-----SV-----
Consensus (351) PDKR I DE
421                                     490
humPMS2 (408) TGEKKDVSISRLEAFSLRHTTENKPHSPKTPPRRSPLGQKRGMLSSSTSGAISDKGVIRPQKEAVSS
AtPMS2 (328) -----IGSLREGLNEIYSSSNASYIVNRFENSEQPKAGVSSFQKSNLLSEGI VLDVSSKTRLG
Consensus (421) I LREA HSS N H E S ISD VL
491                                     560
humPMS2 (478) SHGPSDPTDRAEVEKSGHGSTSVDSGFSIPDTGSHCSSEYAASSPGRGSGEHVDSQEKAPETDSFS
AtPMS2 (389) EAIEKENPSLRVEIENSSPMEKFKFEIKACGTKKGEGLSVHDVTHLCKTPSKGLPQLNVTEKVTASK
Consensus (491) D EVE D E A S S DK L DA
561                                     630
humPMS2 (548) DVDCHENQEDTGCKERVLPQPTNLATPNTFRFKKEEILSSSDICQKLVNTQDMSASQVDVAVKINKVVP
AtPMS2 (459) DLSSRSS-----FAQSTLNTFVTMGKRHENISTILSETPVLNRQTSSYRVEKSKFEVRLASRCLVE
Consensus (561) DL S F T L K ILS S I S M S DV K LV
631                                     700
humPMS2 (618) LDFSMSSLA KR IQLHHEAQSEEQNYRKFRKICPGENQAAEDLRKEISKTMFAEMEIIIGQFN LGFI
AtPMS2 (522) GEQLDDMVISKEDMTPSERDSELNRI SPGTOA-----D-----NVERHERVILGQFN LGFI
Consensus (631) D L K E G A M IIGQFN LGFI
701                                     770
humPMS2 (688) ITKNEEIFIVDQHADEKYNFEMLOQHVLQGRILIAFOTNLTA VNEAVLIENLEIFKNGFD FVIDE
AtPMS2 (573) IAKLERDLFIVDQHADEKYNFEMLARSTV LNOQFLQSLNLEISPEEVTVLMHMDIISENGFLLEENP
Consensus (701) I KL DIFIVDQHA DEKNFE L TVLN Q LI P L LS E LI LDI R NGF
771                                     840
humPMS2 (758) NAFVTERAKIISLFTSKNWTFCPOVDDELFMISSPVMCR-----PSRVKQMFASRACK
AtPMS2 (643) SAPPGKHFRIRAIPIYSKNIIFGVEDLKLSTLGENHGECSVASSYKTSKTD SICPSRVRAVLASFACS
Consensus (771) AP KL AIP SKN TFG DL DLI L D G PSRVK M ASRACR
841                                     907
humPMS2 (815) SVMICTALNTSEMKKLITMGMEDHPWNCPHGRPTMRRIANIGVISQN-----
AtPMS2 (713) SVMIGDPRKKNEMQIVEHLADLES PWNCPHGRPTMRRLVDITLLTLPPDDDNVND DDDDDATISLA
Consensus (841) SVMIG L EM KII HLADLD PWNCPHGRPTMRHI L I

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Figure 2. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) amino acid sequences. Similarity is 41.5%; identity is 31.1%. Black boxes show identical residues.

09749601.123800

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humPMS2 (1) -----MERAESSST-----EPAKATKPIDRKSVHOTCSQVLSLSTAVKELVENSIDAGATNIDL 70
AtMLH1 (1) MIDDSSLTAEEMEEESPATIVPREPPKIQRLAESVNVNRIACEIQRPVSAVKELVENSIDADSSISV
Consensus (1) ME ES AT I ID V I AG VI SAVKELVENSIDAS I L

71
humPMS2 (57) KLEKYGVLLIEVSENGCVVEENFEGTLKHTTSKIQBEADLTQVETFGFRGEALSSLCALSDVTISTCH 140
AtMLH1 (71) VVKEGGLKLTQVSDCHETRRDLPIICERHTTSKLTKEEDLFSLSMGFRGEALASMTYVAHVITIT
Consensus (71) LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST

141
humPMS2 (127) ASAKVCTILMFHDNGKIIQKTPYPRRGTTVSVQQLFSTLPVHEFEFRIKKEPAAMVQVLIHAYCTISA 210
AtMLH1 (141) KGQIHGYEVSYRDGVMEHEPKACAAYKCTQIMVENLFYNMIAERTLCNSADDYGGTIVDLISRMATHYN
Consensus (141) G RL F KGT I V NLF L R K Q N DYAKIV LL I

211
humPMS2 (197) GIRVSCNQLGCKKQPVVCTGGSPSIKENIGSVFGQKQLQSHIPFVQLPPSDSVCEEYGLSCSALHNL 280
AtMLH1 (210) NVSFGSKRH---CAVKADVHSVSPSRLDLSIRSVGVSVAKNM---KV--E-----VSSQSSGCT
Consensus (211) I SC G V S SPS D I SVFG LI L LS DA

281
humPMS2 (267) FYISGFISQCTHGVGRSSDTRQFFFINRRPCDPAKVCRLVNEVYHM-YNRHQYPFVVLNLSVDSECVDIN 350
AtMLH1 (264) FDMEGFISNSNYVAKKTIL---VLFINDRLVECSALKRAIEIVPAATLPKASKPFVYMSINLPREHVDIN
Consensus (281) F I GFISN H KS FIN R D A L R I VY K PFV L I L E V D I N

351
humPMS2 (336) VTEDRQIILQEELKLLAVLKTSLIGMFDSDVNKLNVSQQLLDVEGNLIKMHAADELEKPMVEKQDQSPS 420
AtMLH1 (331) IHTTKKVSILNQEIIEIMIQ-----SEVE-----VKLRNANDTRTFQEKVVEYIQ
Consensus (351) I P K K I L III MI S IKL A K E

421
humPMS2 (406) LRTGEEKKCVSISRLREAFSLRHTTENKHSFKTPEPRRSPLCKRGMSSSTSGAISDKGVLRPQKEAV 490
AtMLH1 (377) STLTSQSSSPVSKPSG---QKTKVFNKVMRTDSSDPASRLHAFQPKQSLPDKVSSLSVVRSSV
Consensus (421) K D IS A T P P G A L L K AV

491
humPMS2 (476) SSSHCPSDPTERAEVEKDSGHGSTVDSEGFSPIDTGSCHSSEYAASSPGDRSSQEHVDSQEKAPETDES 560
AtMLH1 (443) RQRNPKETALSSVQE-----LIA--G-----V-DSCCHPMLETVRNCTYVGMADDEV
Consensus (491) P D D A V I S G E V DD

561
humPMS2 (546) FSDVDCHSNQEDIGCKFRVLPQPTNLATPNTNRFFKKEEILSSSDICQKLVTNQDMSAQVDVAVKINKV 630
AtMLH1 (489) FALQYNN---THLYLAN-----VVLNSELMLYQQTERRFAHFNAIQLSDAPLSSELILLALKEEDL
Consensus (561) FA V T SK L N I S S L L L

631
humPMS2 (616) VPLDFSMSSIAKRIKQLHHEAQOQSEGONYRKFRAKICPGENQAAEDELKKEISKTFAEEMIIIGQFNLC 700
AtMLH1 (547) DGNNDTKDDIKERIAEMNTLLKKEKAMLEEYFSVHIDSSANLSRLPVILDQYTPDMDRVPEFL--LCLC
Consensus (631) P S L R I L E AE F I N A I S M E I LG

701
humPMS2 (686) FIITKLNEDIPIVDQHTDEKYNFEMLQOHTVLOQRLIAPQTLNLTAVNEAVIELEIFRKNGFDFVI 770
AtMLH1 (615) NDVEWEDKSCFQGVSAAGNIFYAMHPPLLPNPSGDIQFYSKRGESSQEKSDIEGVDMEDNLDODLLS
Consensus (701) I E A F G I SA A L NLDI D L

771
humPMS2 (756) TENAPVTERAKLISLPTSKNMTFGPQDVDELIFMISDSPGVMCRPSRVKQMFASRACRKSVMITALNTS 840
AtMLH1 (685) EAENAWAS-----EHSIQHVLFPMSRLFKPPASMASNGTFVVASLEKLYKIFERC-----
Consensus (771) D R WS L L M S VK K K

841
humPMS2 (826) EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN 877
AtMLH1 (738) -----
Consensus (841)

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Figure 3. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue MLH1 (AtMLH1) amino acid sequences. Similarity is 30%; identity is 18.4%. Black boxes show identical residues.

humPMS2	(1)	MERAESSSTEPAAKIDRKSVQICSCQVVLSTAWKFLVNSLDAGATNIDLKLDYGVLDIENS	70
AtPMS1	(1)	-----MTTLKLLPEGVRIIMRSEIIMFDMARVDEELVFNSLDAGATKVSIFVGVVSCS-VKIV	
Consensus	(1)	K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D	
humPMS2	(71)	NCCVEEENFEGITLKHHTSKIQEADL-FOVETFGFRGEATSSLCALSDVTISCHASAKVSTELMFDH	140
AtPMS1	(59)	DSGVSRDDLVLGGERATSKPHDTNVEEASETFGFRGEALASISDILLEVRIKAIGRPNSYKVMKG	
Consensus	(71)	G GV D L KH TSK DF L T ETGFRGEALASI IS L I T G R M	
humPMS2	(140)	NGKIIQKTPYPRP-RGTFVSVQQLFSTLPVPHKHEFCRNKKREYAKMVQVLHAYCIISAGI-----	210
AtPMS1	(129)	SKCLHLGIDDDKDSGCTTVTVRLFYSQPVRRNYMQSSPKKVLSEIKKCFRIALVHSNVFSFVLDIESD	
Consensus	(141)	I R GTTVSV LF S PVR K Q KK I L II A I	
humPMS2	(199)	-----RVSCTNQLGQGRQPVVCCGSGPSIKENIESV	280
AtPMS1	(199)	EELFQTNPSSAFSLMRDAGTEAVNSLCKVNVTDGMLNVSGFECADDWPTDQCCRRNRRLQSPFYI	
Consensus	(211)	VS K TG I N G I	
humPMS2	(231)	-----GQKQLQSLIFVQLFSDSVCEYGCSCSDALHNTFYISCFISQCTHVGSRSTTRQF	350
AtPMS1	(269)	LCIACPRRLYEFSEFSPKTHVEKKWGEVLAFLRITANWKKDRILELFDGADILAKDRQDLIDKI	
Consensus	(281)	F S I F P A E LA L G G D	
humPMS2	(290)	FFINR-----RPCDPAVCRLVNEVYHMYNRHQYFVVLNISVSECVDINWTPDKRQIIL	420
AtPMS1	(339)	RLQNGSLFSILHFLDADWPEAMEPPAKKLRKSNHAPCSSLLFESADFKQDGYFSPRKDWSPCEVEL	
Consensus	(351)	N DPAK H FP D V I L	
humPMS2	(346)	QEEKLLAVLKTSLIGMFDSDVNKLNVSCPLLEVEGNLIKMHAADEKPMVEXDQSPSLRGEEKKDV	490
AtPMS1	(409)	KIQNPKEQGTVAGFESRTDSLQSRDIEMTNEFPQVTDLLLETSLVADSKCRKGLTRCQIETPVNINH	
Consensus	(421)	DS LN I Q D L A L KQ S T	
humPMS2	(416)	SISRLREAFS-----LRRTTENKPHSEKTEPRRSPLGQ	560
AtPMS1	(479)	DFMKDSVDLNFQFQGLKDELDVSNICIGKHLRGCSSRVSLTFHEPKLSEVEGYESVVMIEKQSSPRV	
Consensus	(491)	K D L H P P K S	
humPMS2	(450)	KRGLSSITSGAISDKVLRPQKEAVSSSHG--SDPTDFAVEKDSGHGSFVSEGESIPTGSHCSS	630
AtPMS1	(549)	LETREGGYCDVYSDHTPDCLSGSSWQDQTDWFTQCSSDGGGIGEDFNIPITAEEDSYDEKVGSKK	
Consensus	(561)	S SDK A S P SDRA V T IDS F D	
humPMS2	(518)	EYAASSPDRGSQEHVDSOE-----KAEETDSSFDDVCHSNQEDTGCKFRVLQNTLATPNTKRFKKE	700
AtPMS1	(619)	YLSSVNVSSVTGSPCLSEWSPMYSTSATKWBSEYQKGRILEQSLRLGRVDEFCFSAANNIKFDH	
Consensus	(631)	AA G S S E P SD D K LP P S	
humPMS2	(583)	HILSSSIQKLVNTQDMSASQVDVVKINPK---VPLDFSMSELAIRIKQLHHEAQSSEBNYRK	770
AtPMS1	(689)	HVIPEMCCETGTDSTAIQNTCLQDLKICSSWGHADDVRIDQYIRSEKFSYMDGTNNNAKRSKRS	
Consensus	(701)	EII D C S LA KI K L SI K QN G Q KK	
humPMS2	(649)	RAKICPGENQ-----	840
AtPMS1	(759)	RSAPPFYREKKRFISLSCKSDTKPKNSDPSEPDDECLTQPCNASQMHKCSILDDVSYDHIQETEKRLS	
Consensus	(771)	RA	
humPMS2	(659)	-----	910
AtPMS1	(829)	SASDLKASAGCRTVHSETQDEVDHEDFSSEEFLDPIKSTTKWRHNCAVSQVPKESHELHGQDGVFDISSG	
Consensus	(841)		
humPMS2	(659)	-----AALDELKREISKTMFAEMEIIQGFNLGFIITKLNEDIRIVDQHAIDEKYNFEMLQOHTVLQGGRL	980
AtPMS1	(899)	LLHLRSDSLVPESINRHSLEDAKVLOQVDKKYPIVACGTVALVDQHAADERIRLEELRTKFINALLI	
Consensus	(911)	A E L I K D II Q FI I IVDQHA DEK E L I A I	
humPMS2	(724)	IAPQTLNITAVNEAVIENLEIFRKNCFDFVIDENAPVTERAK-----LISLTSKNWTFGPQ	1050
AtPMS1	(969)	FVLTLKVLPEMGYQLQSYSEIQLDQWICNETVEGSTSFKKNMSSIIQRKPTPITNAVCILGVNLSDV	
Consensus	(981)	L M LL E R GF I A S K L ALP	
humPMS2	(782)	DVDLIFMSSSPGVMCRESRVKQMFASRACRKSVMIETALNTSEMKKLTHMGEMDHPWNCPHGRPTMR	1120
AtPMS1	(1039)	DLLEFLQQAATDGSSTIIPSLRLVNLKACRGATMFDSLLFSECSLIIDGLKQTSCLCFQAGCRPTTV	
Consensus	(1051)	DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT	
humPMS2	(852)	HIANGVISON-----	1164
AtPMS1	(1109)	PLVDLKAHLKQIAKLSGRQVWHGLQRREITLDRAKSLDNAKS-	
Consensus	(1121)	I L I N	

Figure 4. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue PMS1 (AtPMS1) amino acid sequences. Similarity is 24.4%; identity is 15%. Black boxes show identical residues.

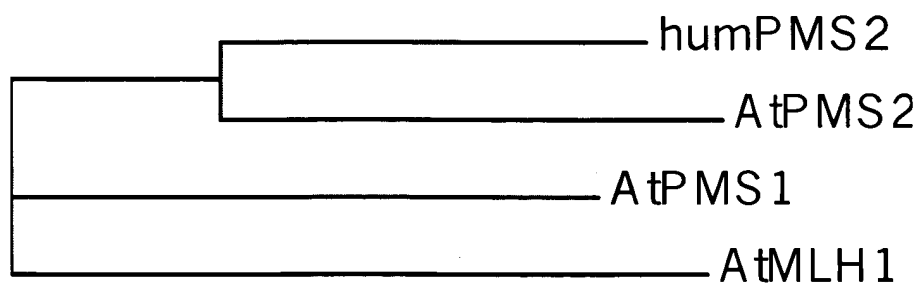


Figure 5. Phylogenetic tree of the *Arabidopsis thaliana* PMS2 gene homologues.

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1                               70
humPMS134 (1) ATGCGCGAGCTGAGAGCTCGAGTACAGAACTGCTAAGGC-----ATCGAACCTATTGATCGGAAGT
AtPMS134 (1) ATGCGAGGAGATTCTTCTCGCTCCGACGACTACTAGCTCTCCTTTGATAAGACCTATAACAGAAACG
Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
71                               140
humPMS134 (65) CAGTCCATCAGATTGCTCTGGCAGCTGGTACTGAGTCTAAGCACTGCGGAAAGGAGTTACTASAAAA
AtPMS134 (71) TAAATTCACAGAACTGTTCGGTCAASTCACTTAGACCTCTCTTGGGCGCAAGGAGCTGTGCSAGAA
Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA
141                               210
humPMS134 (135) CAGTCCGATGCTGCTGCCACTAATATTGATCTAAGCTTAAGGACTATCGAATGGTCTTATTGAAGTT
AtPMS134 (141) TAGTTCGACGCGCGCCACCACTATAGAGATTAACTCCGAGACTACGGCAAGACTATTTTCAGGTC
Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT
211                               280
humPMS134 (205) TCAGACAATGGATGTGGGCT-----AGAAGAAG-----AAACTTCGAAGG-CTTAA-
AtPMS134 (211) ATTGACAATGGTTGTGGCAATTTCCCAACCAATTTCAAGSTTTGTGTCCAATTTC-CCGAAGAACTTTTG
Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT
281                               350
humPMS134 (251) -----CTCTGAACATCAACACATCTAAGATTCAAGAGTTGCGACCTAACTCGGTTGAA-ACTT
AtPMS134 (281) ATGTTCTTGCACTTAAGCATCATACTCTAAATTAGAGGATTCACAGATCTTTTGATTGACTACTT
Consensus (281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT
351                               420
humPMS134 (311) TTGGCTTTCCGGGGAAGCTCTGAGCTCACTTTGTGCACTGACCGATGTCACCAATTCTACCTC--CCAC
AtPMS134 (350) ATGGCTTTTACAGCAAGGCTTGAGCTCTCTCTGTGCACTTGCAGATCTCAGTC--GGAAAGCAACAA
Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A
421                               444
humPMS134 (379) CCATCGGGGAAGGTTGGAAGT---
AtPMS134 (420) CAATGAGGCA--ATTGCTAGGCTC
Consensus (421) G AT GC A GTTG AC

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Figure 6. Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) DNA sequences. Similarity is 53.2%; identity is 53.2%. Black boxes show identical nucleotides.

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1                                     70
humPMS134 (1) --MERAESSSEPAKATKPIDKSVHICSGQVILSLSTAVKELVENS LDAGATNIDLKLDYGVELIEV
AtPMS134 (1) MQGDSSSPPTTSSPLIRPINENVIHRCSGQVILDLSSAVKELVENS LDAGATSEINLRDYGEYFCV
Consensus (1)   D A S S T A I K P I R I H I C S G Q V I L L S S A V K E L V E N S L D A G A T I D I L K D Y G D V
71                                     140
humPMS134 (69) SDNGCGVEEENF-----EGL L K H H T S K I Q E P A D L T Q V E T F G F R G E A L S S L C A L S D V I I S T C H A
AtPMS134 (71) IDNGCGIISPNEKVCVQILRRTFDVLALKHHTSKLEDETD L L N L T Y G F R G E A L S S L C A L G N L V E I R T K
Consensus (71) D N G C G I N F D L L K H H T S K I D F D L N L T F G F R G E A L S S L C A L L T I T
141
humPMS134 (128) SAKVGT
AtPMS134 (141) NEPVAT
Consensus (141) VAT

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Figure 7. Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) amino acid sequences. Similarity is 65.1%; identity is 50.7%. Black boxes show identical residues.

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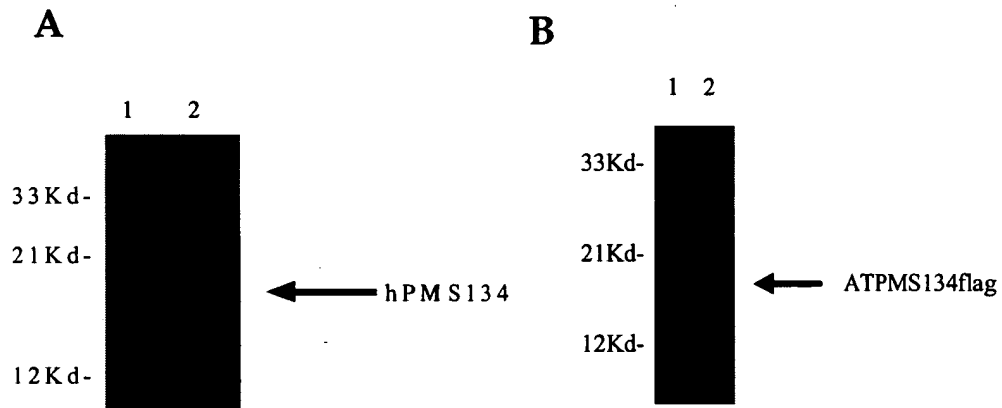


Figure 8: Western blot analysis of bacteria expressing the human PMS134 dominant negative gene (Panel A, lane 2) or the *Arabidopsis thaliana* dominant negative gene (Panel B, lane 2). Panel A, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the human PMS2 N-terminus. Panel B, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the flag epitope placed on the C-terminus of the *Arabidopsis* PMS134 gene. Lane 1 is bacteria containing empty vector as negative control

Dominant Negative Effects of Arabidopsis thaliana PMS2 homolog

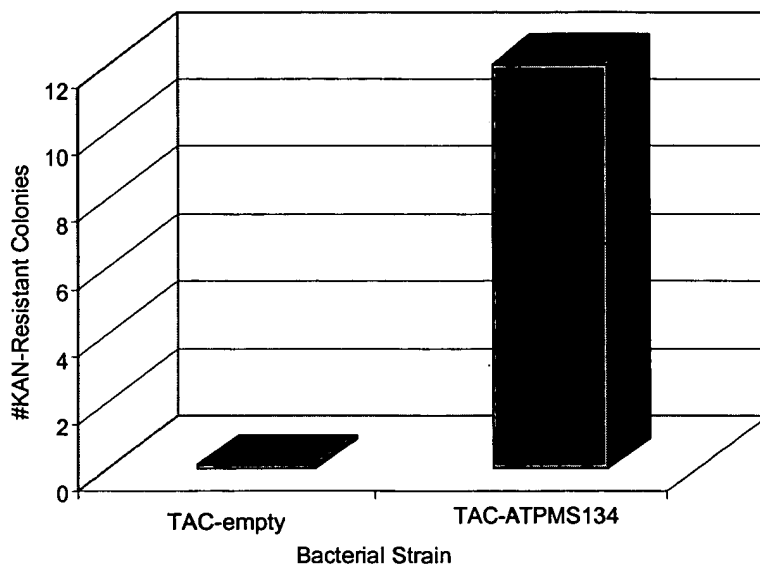


Figure 9. Expression of the *Arabidopsis thaliana* PMS134 gene produces hypermutability in bacteria leading to the generation of new phenotypes. Briefly, bacteria containing the empty vector or the TAC ATPMS134 expression vector were grown and plated on kanamycin containing Lbagar plates. The host bacteria are susceptible to KAN bactericidal activity. Bacterial cultures expressing the hPMS134 gene resulted in genetic alteration of the bacterial host and the generation of clones that are KAN resistant.

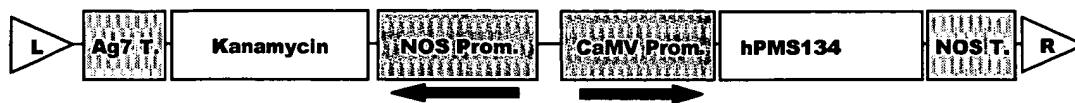


Figure 10. Schematic map of the pCMV-hPMS134-Kan binary plant expression vector. Ag7 T. and NOS T. = gene 7 and Nopaline Synthase poly(A) signals, respectively. NOS Prom and CaMV Prom = Nopaline Synthase and Cauliflower Mosaic Virus promoters, respectively. L and R = left and right T-DNA border repeats, respectively. Arrows indicate direction of transcription.

Western blot analysis showing PMS134 and β-1-tubulin levels. The blot is divided into two main sections, A and B, each with RT+ and RT- lanes. PMS134 is detected in the RT+ lanes (A and B) but not in the RT- lanes. β-1-tubulin is detected in all lanes (A and B, RT+ and RT-), serving as a loading control.

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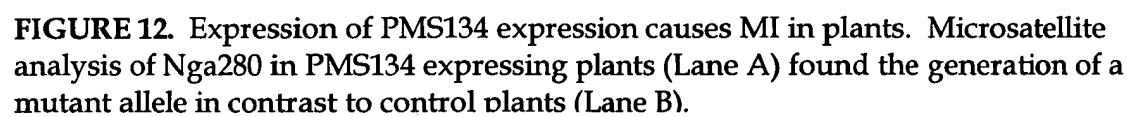


Figure 13. The plant on the left is a wild type *A. thaliana* and the one on the right is MMR defective. Seeds from the MMR defective plant have been obtained and offspring have the same “double-meristem” trait.

